

**09265** **III** **103**

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                                     Met Ser Ser Ser Ser Trp Leu
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Leu Leu Ser Leu Val Ala Val Thr Ala Ala Gln Ser Thr Ile Glu Glu
      10               15               20

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cag gcc aag aca ttt ttg gac aag ttt aac cac gaa gcc gaa gac ctg Gln Ala Lys Thr Phe Leu Asp Lys Phe Asn His Glu Ala Glu Asp Leu 25 30 35	151
ttc tat caa agt tca ctt gct tct tgg aat tat aac acc aat att act Phe Tyr Gln Ser Ser Leu Ala Ser Trp Asn Tyr Asn Thr Asn Ile Thr 40 45 50 55	199
gaa gag aat gtc caa aac atg aat aat gct ggg gac aaa tgg tct gcc Glu Glu Asn Val Gln Asn Met Asn Asn Ala Gly Asp Lys Trp Ser Ala 60 65 70	247
ttt tta aag gaa cag tcc aca ctt gcc caa atg tat cca cta caa gaa Phe Leu Lys Glu Gln Ser Thr Leu Ala Gln Met Tyr Pro Leu Gln Glu 75 80 85	295
att cag aat ctc aca gtc aag ctt cag ctg cag gct ctt cag caa aat Ile Gln Asn Leu Thr Val Lys Leu Gln Leu Gln Ala Leu Gln Gln Asn 90 95 100	343
ggg tct tca gtg ctc tca gaa gac aag agc aaa cgg ttg aac aca att Gly Ser Ser Val Leu Ser Glu Asp Lys Ser Lys Arg Leu Asn Thr Ile 105 110 115	391
cta aat aca atg agc acc atc tac agt act gga aaa gtt tgt aac cca Leu Asn Thr Met Ser Thr Ile Tyr Ser Thr Gly Lys Val Cys Asn Pro 120 125 130 135	439
gat aat cca caa gaa tgc tta tta ctt gaa cca ggt ttg aat gaa ata Asp Asn Pro Gln Glu Cys Leu Leu Leu Glu Pro Gly Leu Asn Glu Ile 140 145 150	487
atg gca aac agt tta gac tac aat gag agg ctc tgg gct tgg gaa agc Met Ala Asn Ser Leu Asp Tyr Asn Glu Arg Leu Trp Ala Trp Glu Ser 155 160 165	535
tgg aga tct gag gtc ggc aag cag ctg agg cca tta tat gaa gag tat Trp Arg Ser Glu Val Gly Lys Gln Leu Arg Pro Leu Tyr Glu Glu Tyr 170 175 180	583
gtg gtc ttg aaa aat gag atg gca aga gca aat cat tat gag gac tat Val Val Leu Lys Asn Glu Met Ala Arg Ala Asn His Tyr Glu Asp Tyr 185 190 195	631

0978385.101604

ggg gat tat tgg aga gga gac tat gaa gta aat ggg gta gat ggc tat	679
Gly Asp Tyr Trp Arg Gly Asp Tyr Glu Val Asn Gly Val Asp Gly Tyr	
200 205 210 215	
gac tac agc cgc ggc cag ttg att gaa gat gtg gaa cat acc ttt gaa	727
Asp Tyr Ser Arg Gly Gln Leu Ile Glu Asp Val Glu His Thr Phe Glu	
220 225 230	
gag att aaa cca tta tat gaa cat ctt cat gcc tat gtg agg gca aag	775
Glu Ile Lys Pro Leu Tyr Glu His Leu His Ala Tyr Val Arg Ala Lys	
235 240 245	
ttg atg aat gcc tat cct tcc tat atc agt cca att gga tgc ctc cct	823
Leu Met Asn Ala Tyr Pro Ser Tyr Ile Ser Pro Ile Gly Cys Leu Pro	
250 255 260	
gct cat ttg ctt ggt gat atg tgg ggt aga ttt tgg aca aat ctg tac	871
Ala His Leu Leu Gly Asp Met Trp Gly Arg Phe Trp Thr Asn Leu Tyr	
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tct ttg aca gtt ccc ttt gga cag aaa cca aac ata gat gtt act gat	919
Ser Leu Thr Val Pro Phe Gly Gln Lys Pro Asn Ile Asp Val Thr Asp	
280 285 290 295	
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Ala Met Val Asp Gln Ala Trp Asp Ala Gln Arg Ile Phe Lys Glu Ala	
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Glu Lys Phe Phe Val Ser Val Gly Leu Pro Asn Met Thr Gln Gly Phe	
315 320 325	
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Trp Glu Asn Ser Met Leu Thr Asp Pro Gly Asn Val Gln Lys Ala Val	
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tgc cat ccc aca gct tgg gac ctg ggg aag ggc gac ttc agg atc ctt	1111
Cys His Pro Thr Ala Trp Asp Leu Gly Lys Gly Asp Phe Arg Ile Leu	
345 350 355	
atg tgc aca aag gtg aca atg gac gac ttc ctg aca gct cat cat gag	1159

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Met Cys Thr Lys Val Thr Met Asp Asp Phe Leu Thr Ala His His Glu  
 360 365 370 375

atg ggg cat atc cag tat gat atg gca tat gct gca caa cct ttt ctg 1207  
 Met Gly His Ile Gln Tyr Asp Met Ala Tyr Ala Ala Gln Pro Phe Leu  
 380 385 390

cta aga aat gga gct aat gaa gga ttc cat gaa gct gtt ggg gaa atc 1255  
 Leu Arg Asn Gly Ala Asn Glu Gly Phe His Glu Ala Val Gly Glu Ile  
 395 400 405

atg tca ctt tct gca gcc aca cct aag cat tta aaa tcc att ggt ctt 1303  
 Met Ser Leu Ser Ala Ala Thr Pro Lys His Leu Lys Ser Ile Gly Leu  
 410 415 420

ctg tca ccc gat ttt caa gaa gac aat gaa aca gaa ata aac ttc ctg 1351  
 Leu Ser Pro Asp Phe Gln Glu Asp Asn Glu Thr Glu Ile Asn Phe Leu  
 425 430 435

ctc aaa caa gca ctc acg att gtt ggg act ctg cca ttt act tac atg 1399  
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tta gag aag tgg agg tgg atg gtc ttt aaa ggg gaa att ccc aaa gac 1447  
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cag tgg atg aaa aag tgg tgg gag atg aag cga gag ata gtt ggg gtg 1495  
 Gln Trp Met Lys Lys Trp Trp Glu Met Lys Arg Glu Ile Val Gly Val  
 475 480 485

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 Val Glu Pro Val Pro His Asp Glu Thr Tyr Cys Asp Pro Ala Ser Leu  
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 Phe His Val Ser Asn Asp Tyr Ser Phe Ile Arg Tyr Tyr Thr Arg Thr  
 505 510 515

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 520 525 530 535

00973335-101601

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Glu Gly Pro Leu His Lys Cys Asp Ile Ser Asn Ser Thr Glu Ala Gly	
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Gln Lys Leu Phe Asn Met Leu Arg Leu Gly Lys Ser Glu Pro Trp Thr	
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cta gca ttg gaa aat gtt gta gga gca aag aac atg aat gta agg cca	1783
Leu Ala Leu Glu Asn Val Val Gly Ala Lys Asn Met Asn Val Arg Pro	
570 575 580	
ctg ctc aac tac ttt gag ccc tta ttt acc tgg ctg aaa gac cag aac	1831
Leu Leu Asn Tyr Phe Glu Pro Leu Phe Thr Trp Leu Lys Asp Gln Asn	
585 590 595	
aag aat tct ttt gtg gga tgg agt acc gac tgg agt cca tat gca gac	1879
Lys Asn Ser Phe Val Gly Trp Ser Thr Asp Trp Ser Pro Tyr Ala Asp	
600 605 610 615	
caa agc atc aaa gtg agg ata agc cta aaa tca gct ctt gga gat aaa	1927
Gln Ser Ile Lys Val Arg Ile Ser Leu Lys Ser Ala Leu Gly Asp Lys	
620 625 630	
gca tat gaa tgg aac gac aat gaa atg tac ctg ttc cga tca tct gtt	1975
Ala Tyr Glu Trp Asn Asp Asn Glu Met Tyr Leu Phe Arg Ser Ser Val	
635 640 645	
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Ala Tyr Ala Met Arg Gln Tyr Phe Leu Lys Val Lys Asn Gln Met Ile	
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Ser Phe Asn Phe Phe Val Thr Ala Pro Lys Asn Val Ser Asp Ile Ile	
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cct aga act gaa gtt gaa aag gcc atc agg atg tcc cgg agc cgt atc	2167

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Pro Arg Thr Glu Val Glu Lys Ala Ile Arg Met Ser Arg Ser Arg Ile	
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Asn Asp Ala Phe Arg Leu Asn Asp Asn Ser Leu Glu Phe Leu Gly Ile	
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cag cca aca ctt gga cct cct aac cag ccc cct gtt tcc ata tgg ctg	2263
Gln Pro Thr Leu Gly Pro Pro Asn Gln Pro Pro Val Ser Ile Trp Leu	
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Leu Ile Phe Thr Gly Ile Arg Asp Arg Lys Lys Lys Asn Lys Ala Arg	
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Ser Gly Glu Asn Pro Tyr Ala Ser Ile Asp Ile Ser Lys Gly Glu Asn	
780 785 790	
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Asn Pro Gly Phe Gln Asn Thr Asp Asp Val Gln Thr Ser Phe	
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<210> 2  
 <211> 805  
 <212> PRT  
 <213> Homo sapiens

<400> 2

Met	Ser	Ser	Ser	Ser	Trp	Leu	Leu	Leu	Ser	Leu	Val	Ala	Val	Thr	Ala
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Ala	Gln	Ser	Thr	Ile	Glu	Glu	Gln	Ala	Lys	Thr	Phe	Leu	Asp	Lys	Phe
			20					25					30		
Asn	His	Glu	Ala	Glu	Asp	Leu	Phe	Tyr	Gln	Ser	Ser	Leu	Ala	Ser	Trp
		35				40						45			
Asn	Tyr	Asn	Thr	Asn	Ile	Thr	Glu	Glu	Asn	Val	Gln	Asn	Met	Asn	Asn
	50				55					60					
Ala	Gly	Asp	Lys	Trp	Ser	Ala	Phe	Leu	Lys	Glu	Gln	Ser	Thr	Leu	Ala
65				70					75					80	
Gln	Met	Tyr	Pro	Leu	Gln	Glu	Ile	Gln	Asn	Leu	Thr	Val	Lys	Leu	Gln
			85					90					95		
Leu	Gln	Ala	Leu	Gln	Gln	Asn	Gly	Ser	Ser	Val	Leu	Ser	Glu	Asp	Lys
		100					105						110		
Ser	Lys	Arg	Leu	Asn	Thr	Ile	Leu	Asn	Thr	Met	Ser	Thr	Ile	Tyr	Ser
		115				120						125			
Thr	Gly	Lys	Val	Cys	Asn	Pro	Asp	Asn	Pro	Gln	Glu	Cys	Leu	Leu	Leu
	130					135					140				
Glu	Pro	Gly	Leu	Asn	Glu	Ile	Met	Ala	Asn	Ser	Leu	Asp	Tyr	Asn	Glu
145				150						155				160	
Arg	Leu	Trp	Ala	Trp	Glu	Ser	Trp	Arg	Ser	Glu	Val	Gly	Lys	Gln	Leu
			165					170						175	
Arg	Pro	Leu	Tyr	Glu	Glu	Tyr	Val	Val	Leu	Lys	Asn	Glu	Met	Ala	Arg
		180					185					190			
Ala	Asn	His	Tyr	Glu	Asp	Tyr	Gly	Asp	Tyr	Trp	Arg	Gly	Asp	Tyr	Glu
		195					200					205			
Val	Asn	Gly	Val	Asp	Gly	Tyr	Asp	Tyr	Ser	Arg	Gly	Gln	Leu	Ile	Glu
	210					215					220				
Asp	Val	Glu	His	Thr	Phe	Glu	Glu	Ile	Lys	Pro	Leu	Tyr	Glu	His	Leu
225				230						235				240	
His	Ala	Tyr	Val	Arg	Ala	Lys	Leu	Met	Asn	Ala	Tyr	Pro	Ser	Tyr	Ile
			245					250						255	
Ser	Pro	Ile	Gly	Cys	Leu	Pro	Ala	His	Leu	Leu	Gly	Asp	Met	Trp	Gly
		260					265						270		
Arg	Phe	Trp	Thr	Asn	Leu	Tyr	Ser	Leu	Thr	Val	Pro	Phe	Gly	Gln	Lys
		275					280						285		

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Pro Asn Ile Asp Val Thr Asp Ala Met Val Asp Gln Ala Trp Asp Ala  
 290 295 300  
 Gln Arg Ile Phe Lys Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu  
 305 310 315 320  
 Pro Asn Met Thr Gln Gly Phe Trp Glu Asn Ser Met Leu Thr Asp Pro  
 325 330 335  
 Gly Asn Val Gln Lys Ala Val Cys His Pro Thr Ala Trp Asp Leu Gly  
 340 345 350  
 Lys Gly Asp Phe Arg Ile Leu Met Cys Thr Lys Val Thr Met Asp Asp  
 355 360 365  
 Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala  
 370 375 380  
 Tyr Ala Ala Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe  
 385 390 395 400  
 His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys  
 405 410 415  
 His Leu Lys Ser Ile Gly Leu Leu Ser Pro Asp Phe Gln Glu Asp Asn  
 420 425 430  
 Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly  
 435 440 445  
 Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe  
 450 455 460  
 Lys Gly Glu Ile Pro Lys Asp Gln Trp Met Lys Lys Trp Trp Glu Met  
 465 470 475 480  
 Lys Arg Glu Ile Val Gly Val Val Glu Pro Val Pro His Asp Glu Thr  
 485 490 495  
 Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe  
 500 505 510  
 Ile Arg Tyr Tyr Thr Arg Thr Leu Tyr Gln Phe Gln Phe Gln Glu Ala  
 515 520 525  
 Leu Cys Gln Ala Ala Lys His Glu Gly Pro Leu His Lys Cys Asp Ile  
 530 535 540  
 Ser Asn Ser Thr Glu Ala Gly Gln Lys Leu Phe Asn Met Leu Arg Leu  
 545 550 555 560  
 Gly Lys Ser Glu Pro Trp Thr Leu Ala Leu Glu Asn Val Val Gly Ala  
 565 570 575  
 Lys Asn Met Asn Val Arg Pro Leu Leu Asn Tyr Phe Glu Pro Leu Phe  
 580 585 590  
 Thr Trp Leu Lys Asp Gln Asn Lys Asn Ser Phe Val Gly Trp Ser Thr  
 595 600 605  
 Asp Trp Ser Pro Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu  
 610 615 620

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Lys Ser Ala Leu Gly Asp Lys Ala Tyr Glu Trp Asn Asp Asn Glu Met  
 625 630 635 640  
 Tyr Leu Phe Arg Ser Ser Val Ala Tyr Ala Met Arg Gln Tyr Phe Leu  
 645 650 655  
 Lys Val Lys Asn Gln Met Ile Leu Phe Gly Glu Glu Asp Val Arg Val  
 660 665 670  
 Ala Asn Leu Lys Pro Arg Ile Ser Phe Asn Phe Phe Val Thr Ala Pro  
 675 680 685  
 Lys Asn Val Ser Asp Ile Ile Pro Arg Thr Glu Val Glu Lys Ala Ile  
 690 695 700  
 Arg Met Ser Arg Ser Arg Ile Asn Asp Ala Phe Arg Leu Asn Asp Asn  
 705 710 715 720  
 Ser Leu Glu Phe Leu Gly Ile Gln Pro Thr Leu Gly Pro Pro Asn Gln  
 725 730 735  
 Pro Pro Val Ser Ile Trp Leu Ile Val Phe Gly Val Val Met Gly Val  
 740 745 750  
 Ile Val Val Gly Ile Val Ile Leu Ile Phe Thr Gly Ile Arg Asp Arg  
 755 760 765  
 Lys Lys Lys Asn Lys Ala Arg Ser Gly Glu Asn Pro Tyr Ala Ser Ile  
 770 775 780  
 Asp Ile Ser Lys Gly Glu Asn Asn Pro Gly Phe Gln Asn Thr Asp Asp  
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 Val Gln Thr Ser Phe  
 805

<210> 3  
 <211> 2415  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> This degenerate sequence encodes the amino acid  
 sequence of SEQ ID NO:2.

<221> misc\_feature  
 <222> (1)...(2415)  
 <223> n = A,T,C or G

<400> 3

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taycarwsnw snytngcnws ntggaaytay aayacnaaya thacngarga raaygtncar	180
aayatgaaya aygcnggnga yaartggwsn gcnttyytna argarcarws nacnytngcn	240

caratgtayc	cnytnarga	rathcaraay	ytnacngtna	arytnaryt	ncargcnytn	300
carcaraayg	gnwsnwsngt	nytnwsngar	gayaarwsna	armgnytnaa	yacnathytn	360
aayacnatgw	snacnathta	ywsnacnggn	aargtntgya	ayccngayaa	yccncargar	420
tgyytnytny	tngarccngg	nytnaaygar	athatggcna	aywsnytnga	ytayaaygar	480
mgnytnntggg	cntgggarws	ntggmgwnsn	gargtnggna	arcarytnmg	nccnytnntay	540
gargartayg	tngtnytnaa	raaygaratg	gcnmgngcna	aycaytayga	rgaytayggg	600
gaytaytgmm	gnngngayta	ygargtnaay	ggngtngayg	gntaygayta	ywsnmngngn	660
carytnathg	argaygtnga	rcayacntty	gargaratha	arccnytnnta	ygarcaaytn	720
caygcntayg	tnmgngcnaa	rytnatgaay	gcntayccnw	sntayathws	nccnathggg	780
tgyytnccng	cncayytnyt	ngngngaytg	tggggngmgnt	tytggaacnaa	yytnntaywsn	840
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caratgathy	tnnttyggnga	rgargaygt	mgngtngcna	ayytnaarcc	nmgnathwsn	2040
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garaargcna	thmgntatgws	nmgnwsnmgn	athaaygayg	cnttymgnyt	naaygayaay	2160
wsnytngart	tyytnngnat	hcarccnacn	ytnggncnc	cnaaycarcc	nccngtnwsn	2220
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&lt;210&gt; 4

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

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&lt;220&gt;

&lt;223&gt; Peptide linker

&lt;400&gt; 4

Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
 1 5 10 15

&lt;210&gt; 5

&lt;211&gt; 2638

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (106)...(2520)

&lt;400&gt; 5

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 Met Ser Ser Ser  
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tcc tgg ctc ctt ctc agc ctt gtt gct gtt act act gct cag tcc ctc 165  
 Ser Trp Leu Leu Leu Ser Leu Val Ala Val Thr Thr Ala Gln Ser Leu  
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acc gag gaa aat gcc aag aca ttt tta aac aac ttt aat cag gaa gct 213  
 Thr Glu Glu Asn Ala Lys Thr Phe Leu Asn Asn Phe Asn Gln Glu Ala  
 25 30 35

gaa gac ctg tct tat caa agt tca ctt gct tct tgg aat tat aat act 261  
 Glu Asp Leu Ser Tyr Gln Ser Ser Leu Ala Ser Trp Asn Tyr Asn Thr  
 40 45 50

aac att act gaa gaa aat gcc caa aag atg agt gag gct gca gcc aaa 309  
 Asn Ile Thr Glu Glu Asn Ala Gln Lys Met Ser Glu Ala Ala Ala Lys  
 55 60 65

tgg tct gcc ttt tat gaa gaa cag tct aag act gcc caa agt ttc tca 357  
 Trp Ser Ala Phe Tyr Glu Glu Gln Ser Lys Thr Ala Gln Ser Phe Ser  
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cta caa gaa atc cag act ccg atc atc aag cgt caa cta cag gcc ctt 405

09978385-101601

Leu Gln Glu Ile Gln Thr Pro Ile Ile Lys Arg Gln Leu Gln Ala Leu	
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Gln Gln Ser Gly Ser Ser Ala Leu Ser Ala Asp Lys Asn Lys Gln Leu	
105 110 115	
aac aca att ctg aac acc atg agc acc att tac agt act gga aaa gtt	501
Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser Thr Gly Lys Val	
120 125 130	
tgc aac cca aag aac cca caa gaa tgc tta tta ctt gag cca gga ttg	549
Cys Asn Pro Lys Asn Pro Gln Glu Cys Leu Leu Leu Glu Pro Gly Leu	
135 140 145	
gat gaa ata atg gcg aca agc aca gac tac aac tct agg ctc tgg gca	597
Asp Glu Ile Met Ala Thr Ser Thr Asp Tyr Asn Ser Arg Leu Trp Ala	
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Trp Glu Gly Trp Arg Ala Glu Val Gly Lys Gln Leu Arg Pro Leu Tyr	
165 170 175 180	
gaa gag tat gtg gtc ctg aaa aac gag atg gca aga gca aac aat tat	693
Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg Ala Asn Asn Tyr	
185 190 195	
aac gac tat ggg gat tat tgg aga ggg gac tat gaa gca gag gga gca	741
Asn Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu Ala Glu Gly Ala	
200 205 210	
gat ggc tac aac tat aac cgt aac cag ttg att gaa gat gta gaa cgt	789
Asp Gly Tyr Asn Tyr Asn Arg Asn Gln Leu Ile Glu Asp Val Glu Arg	
215 220 225	
acc ttc gca gag atc aag cca ttg tat gag cat ctt cat gcc tat gtg	837
Thr Phe Ala Glu Ile Lys Pro Leu Tyr Glu His Leu His Ala Tyr Val	
230 235 240	
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Arg Arg Lys Leu Met Asp Thr Tyr Pro Ser Tyr Ile Ser Pro Thr Gly	
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097335-101601

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gtt act gat gca atg atg aat cag ggc tgg gat gca gaa agg ata ttt Val Thr Asp Ala Met Met Asn Gln Gly Trp Asp Ala Glu Arg Ile Phe 295 300 305	1029
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cat cac gag atg gga cac atc caa tat gac atg gca tat gcc agg caa His His Glu Met Gly His Ile Gln Tyr Asp Met Ala Tyr Ala Arg Gln 375 380 385	1269
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gga gaa atc atg tca ctt tct gca gct acc ccc aag cat ctg aaa tcc Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys His Leu Lys Ser 405 410 415 420	1365
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 Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe Arg Gly Glu Ile  
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ccc aaa gag cag tgg atg aaa aag tgg tgg gag atg aag cgg gag atc 1557  
 Pro Lys Glu Gln Trp Met Lys Lys Trp Trp Glu Met Lys Arg Glu Ile  
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gtt ggt gtg gtg gag cct ctg cct cat gat gaa aca tac tgt gac cct 1605  
 Val Gly Val Val Glu Pro Leu Pro His Asp Glu Thr Tyr Cys Asp Pro  
 485 490 495 500

gca tct ctg ttc cat gtt tct aat gat tac tca ttc att cga tat tac 1653  
 Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe Ile Arg Tyr Tyr  
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 Thr Arg Thr Ile Tyr Gln Phe Gln Phe Gln Glu Ala Leu Cys Gln Ala  
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 Val Lys Pro Leu Leu Asn Tyr Phe Gln Pro Leu Phe Asp Trp Leu Lys  
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tat gcc gac caa agc att aaa gtg agg ata agc cta aaa tca gct ctt	1989
Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu Lys Ser Ala Leu	
615 620 625	
gga gct aat gca tat gaa tgg acc aac aac gaa atg ttc ctg ttc cga	2037
Gly Ala Asn Ala Tyr Glu Trp Thr Asn Asn Glu Met Phe Leu Phe Arg	
630 635 640	
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Ser Ser Val Ala Tyr Ala Met Arg Lys Tyr Phe Ser Ile Ile Lys Asn	
645 650 655 660	
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Gln Thr Val Pro Phe Leu Glu Glu Asp Val Arg Val Ser Asp Leu Lys	
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cca aga gtc tcc ttc tac ttc ttt gtc acc tca ccc caa aat gtg tct	2181
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Asp Val Ile Pro Arg Ser Glu Val Glu Asp Ala Ile Arg Met Ser Arg	
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Gly Arg Ile Asn Asp Val Phe Gly Leu Asn Asp Asn Ser Leu Glu Phe	
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Leu Gly Ile His Pro Thr Leu Glu Pro Pro Tyr Gln Pro Pro Val Thr	
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ata tgg ctg att att ttt ggt gtt gtg atg gca ctg gta gtg gtt ggc	2373
Ile Trp Leu Ile Ile Phe Gly Val Val Met Ala Leu Val Val Val Gly	
745 750 755	
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097335-101601

Ile Ile Ile Leu Ile Val Thr Gly Ile Lys Gly Arg Lys Lys Lys Asn  
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 Glu Thr Lys Arg Glu Glu Asn Pro Tyr Asp Ser Met Asp Ile Gly Lys  
 775 780 785

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 790 795 800

ttt tagcaaagca cttgtcatct tcctgtatgt aaatgctaac ttcatagtac 2570  
 Phe  
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 35 40 45  
 Asn Tyr Asn Thr Asn Ile Thr Glu Glu Asn Ala Gln Lys Met Ser Glu  
 50 55 60  
 Ala Ala Ala Lys Trp Ser Ala Phe Tyr Glu Glu Gln Ser Lys Thr Ala  
 65 70 75 80  
 Gln Ser Phe Ser Leu Gln Glu Ile Gln Thr Pro Ile Ile Lys Arg Gln  
 85 90 95  
 Leu Gln Ala Leu Gln Gln Ser Gly Ser Ser Ala Leu Ser Ala Asp Lys  
 100 105 110  
 Asn Lys Gln Leu Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser  
 115 120 125

05978385-101601



Thr Gly Lys Val Cys Asn Pro Lys Asn Pro Gln Glu Cys Leu Leu Leu  
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 165 170 175  
 Arg Pro Leu Tyr Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg  
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 Ala Asn Asn Tyr Asn Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu  
 195 200 205  
 Ala Glu Gly Ala Asp Gly Tyr Asn Tyr Asn Arg Asn Gln Leu Ile Glu  
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 Asp Val Glu Arg Thr Phe Ala Glu Ile Lys Pro Leu Tyr Glu His Leu  
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 His Ala Tyr Val Arg Arg Lys Leu Met Asp Thr Tyr Pro Ser Tyr Ile  
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 Ser Pro Thr Gly Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly  
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 Arg Phe Trp Thr Asn Leu Tyr Pro Leu Thr Val Pro Phe Ala Gln Lys  
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 Pro Asn Ile Asp Val Thr Asp Ala Met Met Asn Gln Gly Trp Asp Ala  
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 Glu Arg Ile Phe Gln Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu  
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 Pro His Met Thr Gln Gly Phe Trp Ala Asn Ser Met Leu Thr Glu Pro  
 325 330 335  
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 340 345 350  
 His Gly Asp Phe Arg Ile Lys Met Cys Thr Lys Val Thr Met Asp Asn  
 355 360 365  
 Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala  
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 Tyr Ala Arg Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe  
 385 390 395 400  
 His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys  
 405 410 415  
 His Leu Lys Ser Ile Gly Leu Leu Pro Ser Asp Phe Gln Glu Asp Ser  
 420 425 430  
 Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly  
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Arg Gly Glu Ile Pro Lys Glu Gln Trp Met Lys Lys Trp Trp Glu Met  
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 485 490 495  
 Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe  
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 Leu Cys Gln Ala Ala Lys Tyr Asn Gly Ser Leu His Lys Cys Asp Ile  
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 Ser Asn Ser Thr Glu Ala Gly Gln Lys Leu Leu Lys Met Leu Ser Leu  
 545 550 555 560  
 Gly Asn Ser Glu Pro Trp Thr Lys Ala Leu Glu Asn Val Val Gly Ala  
 565 570 575  
 Arg Asn Met Asp Val Lys Pro Leu Leu Asn Tyr Phe Gln Pro Leu Phe  
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 Asp Trp Leu Lys Glu Gln Asn Arg Asn Ser Phe Val Gly Trp Asn Thr  
 595 600 605  
 Glu Trp Ser Pro Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu  
 610 615 620  
 Lys Ser Ala Leu Gly Ala Asn Ala Tyr Glu Trp Thr Asn Asn Glu Met  
 625 630 635 640  
 Phe Leu Phe Arg Ser Ser Val Ala Tyr Ala Met Arg Lys Tyr Phe Ser  
 645 650 655  
 Ile Ile Lys Asn Gln Thr Val Pro Phe Leu Glu Glu Asp Val Arg Val  
 660 665 670  
 Ser Asp Leu Lys Pro Arg Val Ser Phe Tyr Phe Phe Val Thr Ser Pro  
 675 680 685  
 Gln Asn Val Ser Asp Val Ile Pro Arg Ser Glu Val Glu Asp Ala Ile  
 690 695 700  
 Arg Met Ser Arg Gly Arg Ile Asn Asp Val Phe Gly Leu Asn Asp Asn  
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 Ser Leu Glu Phe Leu Gly Ile His Pro Thr Leu Glu Pro Pro Tyr Gln  
 725 730 735  
 Pro Pro Val Thr Ile Trp Leu Ile Ile Phe Gly Val Val Met Ala Leu  
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 Val Val Val Gly Ile Ile Ile Leu Ile Val Thr Gly Ile Lys Gly Arg  
 755 760 765  
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00070305 101601

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sequence of SEQ ID NO:6.

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taycarwsnw	snytngcnws	ntggaaytay	aayacnaaya	thacngarga	raaygcncar	180
aaratgwsng	argcngcngc	naartggwsn	gcnttytayg	argarcarws	naaracngcn	240
carwsnttyw	snytncarga	rathcaracn	ccnathatha	armgncaryt	ncargcnytn	300
carcarwsng	gnwsnwsngc	nytnwsngcn	gayaaraaya	arcarytnaa	yacnathytn	360
aayacnatgw	snacnathta	ywsnacnggn	aargtntgya	ayccnaaraa	yccncargar	420
tgyytntytny	tngarccngg	nytngaygar	athatggcna	cnwsnacnga	ytayaaywsn	480
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 Met Ser Ser Ser  
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tcc tgg ctc ctt ctc agc ctt gtt gct gtt act act gct cag tcc ctc 165  
 Ser Trp Leu Leu Leu Ser Leu Val Ala Val Thr Thr Ala Gln Ser Leu  
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acc gag gaa aat gcc aag aca ttt tta aac aac ttt aat cag gag gct 213  
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gaa gac ctg tct tat caa agt tca ctt gct tct tgg aat tat aat act 261  
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aac att act gaa gaa aat gcc caa aag atg agt gag gct gca gcc aaa Asn Ile Thr Glu Glu Asn Ala Gln Lys Met Ser Glu Ala Ala Ala Lys 55 60 65	309
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cta caa gaa atc cag act ccg atc atc aag cgt caa cta cag gcc ctt Leu Gln Glu Ile Gln Thr Pro Ile Ile Lys Arg Gln Leu Gln Ala Leu 85 90 95 100	405
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aac aca att ctg aac acc atg agc acc att tac agt act gga aaa gtt Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser Thr Gly Lys Val 120 125 130	501
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tgg gag ggc tgg agg gct gag gtt ggc aag cag ctg agg ccg ttg tat Trp Glu Gly Trp Arg Ala Glu Val Gly Lys Gln Leu Arg Pro Leu Tyr 165 170 175 180	645
gaa gag tat gtg gtc ctg aaa aac gag atg gca aga gca aac aat tat Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg Ala Asn Asn Tyr 185 190 195	693
aac gac tat ggg gat tat tgg aga ggg gac tat gaa gca gag gga gca Asn Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu Ala Glu Gly Ala 200 205 210	741
gat ggc tac aac tat aac cgt aac cag ttg att gaa gat gta gaa cgt	789

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Asp Gly Tyr Asn Tyr Asn Arg Asn Gln Leu Ile Glu Asp Val Glu Arg	
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Thr Phe Ala Glu Ile Lys Pro Leu Tyr Glu His Leu His Ala Tyr Val	
230 235 240	
agg agg aag ttg atg gat acc tac cct tcc tac atc agc ccc act gga	885
Arg Arg Lys Leu Met Asp Thr Tyr Pro Ser Tyr Ile Ser Pro Thr Gly	
245 250 255 260	
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Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly Arg Phe Trp Thr	
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Gln Gly Phe Trp Ala Asn Ser Met Leu Thr Glu Pro Ala Asp Gly Arg	
325 330 335 340	
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Lys Val Val Cys His Pro Thr Ala Trp Asp Leu Gly His Gly Asp Phe	
345 350 355	
aga atc aag atg tgt aca aag gtc aca atg gac aac ttc ttg aca gcc	1221
Arg Ile Lys Met Cys Thr Lys Val Thr Met Asp Asn Phe Leu Thr Ala	
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cat cac gag atg gga cac atc caa tat gac atg gca tat gcc agg caa	1269

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His His Glu Met Gly His Ile Gln Tyr Asp Met Ala Tyr Ala Arg Gln  
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 gga gaa atc atg tca ctt tct gca gct acc ccc aag cat ctg aaa tcc 1365  
 Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys His Leu Lys Ser  
 405 410 415 420  
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 Ile Gly Leu Leu Pro Ser Asp Phe Gln Glu Asp Ser Glu Thr Glu Ile  
 425 430 435  
 aac ttc cta ctg aaa cag gca ttg aca att gtt gga aca cta ccg ttt 1461  
 Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly Thr Leu Pro Phe  
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 Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe Arg Gly Glu Ile  
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 ccc aaa gag cag tgg atg aaa aag tgg tgg gag atg aag cgg gag atc 1557  
 Pro Lys Glu Gln Trp Met Lys Lys Trp Trp Glu Met Lys Arg Glu Ile  
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 gtt ggt gtg gtg gag cct ctg cct cgt gat gaa aca tac tgt gac cct 1605  
 Val Gly Val Val Glu Pro Leu Pro Arg Asp Glu Thr Tyr Cys Asp Pro  
 485 490 495 500  
 gca tct ctg ttc cat gtt tct aat gat tac tca ttc att cga tat tac 1653  
 Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe Ile Arg Tyr Tyr  
 505 510 515  
 aca agg acc att tac caa ttc cag ttt caa gaa gct ctt tgt caa gca 1701  
 Thr Arg Thr Ile Tyr Gln Phe Gln Phe Gln Glu Ala Leu Cys Gln Ala  
 520 525 530  
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Ala Lys Tyr Asn Gly Ser Leu His Lys Cys Asp Ile Ser Asn Ser Thr	
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gaa gct ggg cag aag ttg ctc aag atg ctg agt ctt gga aat tca gag	1797
Glu Ala Gly Gln Lys Leu Leu Lys Met Leu Ser Leu Gly Asn Ser Glu	
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ccc tgg acc gaa gcc ttg gaa aat gtg gta gga gca agg aat atg gat	1845
Pro Trp Thr Glu Ala Leu Glu Asn Val Val Gly Ala Arg Asn Met Asp	
565 570 575 580	
gta aaa cca ctg ctc aat tac ttc caa ccg ttg ttt gac tgg ctg aaa	1893
Val Lys Pro Leu Leu Asn Tyr Phe Gln Pro Leu Phe Asp Trp Leu Lys	
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gag cag aac aga aat tct ttt gtg ggg tgg aac act gaa tgg agc cca	1941
Glu Gln Asn Arg Asn Ser Phe Val Gly Trp Asn Thr Glu Trp Ser Pro	
600 605 610	
tat gcc gac caa agc att aaa gtg agg ata agc cta aaa tca gct ctt	1989
Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu Lys Ser Ala Leu	
615 620 625	
gga gct aat gca tat gaa tgg acc aac aac gaa atg ttc ctg ttc cga	2037
Gly Ala Asn Ala Tyr Glu Trp Thr Asn Asn Glu Met Phe Leu Phe Arg	
630 635 640	
tca tct gtt gca tat gcc atg aga aag tat tct tca ata atc aaa aac	2085
Ser Ser Val Ala Tyr Ala Met Arg Lys Tyr Ser Ser Ile Ile Lys Asn	
645 650 655 660	
cag aca gtt cct ttt cta gag gaa gat gta cga gtg agt gat ttg aaa	2133
Gln Thr Val Pro Phe Leu Glu Glu Asp Val Arg Val Ser Asp Leu Lys	
665 670 675	
cca aga gtc tcc ttc tac ttc ttt gtc acc tca ccc caa aat gtg tct	2181
Pro Arg Val Ser Phe Tyr Phe Phe Val Thr Ser Pro Gln Asn Val Ser	
680 685 690	
gat gtc att cct aga agt gaa gtt gaa gat gcc atc agg atg tct cgg	2229

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Asp Val Ile Pro Arg Ser Glu Val Glu Asp Ala Ile Arg Met Ser Arg  
 695 700 705

ggc cgc atc aat gat gtc ttt ggc ctg aat gat aac agc ctg gag ttt 2277  
 Gly Arg Ile Asn Asp Val Phe Gly Leu Asn Asp Asn Ser Leu Glu Phe  
 710 715 720

ctg ggg att cac cca aca ctt gag cca cct tac cag cct cct gtc acc 2325  
 Leu Gly Ile His Pro Thr Leu Glu Pro Pro Tyr Gln Pro Pro Val Thr  
 725 730 735 740

ata tgg ctg att att ttt ggt gtt gtg atg gca ctg gta gtg gtt ggc 2373  
 Ile Trp Leu Ile Ile Phe Gly Val Val Met Ala Leu Val Val Val Gly  
 745 750 755

atc atc atc ctg att gtc act ggg atc aaa ggt cga aag aag aaa aat 2421  
 Ile Ile Ile Leu Ile Val Thr Gly Ile Lys Gly Arg Lys Lys Lys Asn  
 760 765 770

gaa aca aaa aga gaa gag aac cct tat gac tcg atg gac att gga aaa 2469  
 Glu Thr Lys Arg Glu Glu Asn Pro Tyr Asp Ser Met Asp Ile Gly Lys  
 775 780 785

gga gaa agc aat gca gga ttc caa aac agt gat gat gct cag act tcc 2517

Gly Glu Ser Asn Ala Gly Phe Gln Asn Ser Asp Asp Ala Gln Thr Ser  
 790 795 800

ttt tagcaaagca cttgtcatct tcctgtatgt aaatgctaac ttcatagtac 2570  
 Phe  
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Ala	Gln	Ser	Leu	Thr	Glu	Glu	Asn	Ala	Lys	Thr	Phe	Leu	Asn	Asn	Phe
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Asn	Tyr	Asn	Thr	Asn	Ile	Thr	Glu	Glu	Asn	Ala	Gln	Lys	Met	Ser	Glu
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Ala	Ala	Ala	Lys	Trp	Ser	Ala	Phe	Tyr	Glu	Glu	Gln	Ser	Lys	Thr	Ala
65					70					75					80
Gln	Ser	Phe	Ser	Leu	Gln	Glu	Ile	Gln	Thr	Pro	Ile	Ile	Lys	Arg	Gln
				85					90					95	
Leu	Gln	Ala	Leu	Gln	Gln	Ser	Gly	Ser	Ser	Ala	Leu	Ser	Ala	Asp	Lys
			100					105					110		
Asn	Lys	Gln	Leu	Asn	Thr	Ile	Leu	Asn	Thr	Met	Ser	Thr	Ile	Tyr	Ser
		115					120					125			
Thr	Gly	Lys	Val	Cys	Asn	Pro	Arg	Asn	Pro	Gln	Glu	Cys	Leu	Leu	Leu
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Glu	Pro	Gly	Leu	Asp	Glu	Ile	Met	Ala	Thr	Ser	Thr	Asp	Tyr	Asn	Ser
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Arg	Leu	Trp	Ala	Trp	Glu	Gly	Trp	Arg	Ala	Glu	Val	Gly	Lys	Gln	Leu
				165					170					175	
Arg	Pro	Leu	Tyr	Glu	Glu	Tyr	Val	Val	Leu	Lys	Asn	Glu	Met	Ala	Arg
			180					185					190		
Ala	Asn	Asn	Tyr	Asn	Asp	Tyr	Gly	Asp	Tyr	Trp	Arg	Gly	Asp	Tyr	Glu
		195					200					205			
Ala	Glu	Gly	Ala	Asp	Gly	Tyr	Asn	Tyr	Asn	Arg	Asn	Gln	Leu	Ile	Glu
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Asp	Val	Glu	Arg	Thr	Phe	Ala	Glu	Ile	Lys	Pro	Leu	Tyr	Glu	His	Leu
225					230					235					240
His	Ala	Tyr	Val	Arg	Arg	Lys	Leu	Met	Asp	Thr	Tyr	Pro	Ser	Tyr	Ile
				245					250					255	
Ser	Pro	Thr	Gly	Cys	Leu	Pro	Ala	His	Leu	Leu	Gly	Asp	Met	Trp	Gly
			260					265					270		
Arg	Phe	Trp	Thr	Asn	Leu	Tyr	Pro	Leu	Thr	Val	Pro	Phe	Ala	Gln	Lys
			275				280					285			
Pro	Asn	Ile	Asp	Val	Thr	Asp	Ala	Met	Met	Asn	Gln	Gly	Trp	Asp	Ala
	290					295					300				
Glu	Arg	Ile	Phe	Gln	Glu	Ala	Glu	Lys	Phe	Phe	Val	Ser	Val	Gly	Leu
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Pro His Met Thr Gln Gly Phe Trp Ala Asn Ser Met Leu Thr Glu Pro  
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 Ala Asp Gly Arg Lys Val Val Cys His Pro Thr Ala Trp Asp Leu Gly  
 340 345 350  
 His Gly Asp Phe Arg Ile Lys Met Cys Thr Lys Val Thr Met Asp Asn  
 355 360 365  
 Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala  
 370 375 380  
 Tyr Ala Arg Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe  
 385 390 395 400  
 His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys  
 405 410 415  
 His Leu Lys Ser Ile Gly Leu Leu Pro Ser Asp Phe Gln Glu Asp Ser  
 420 425 430  
 Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly  
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 Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe  
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 Arg Gly Glu Ile Pro Lys Glu Gln Trp Met Lys Lys Trp Trp Glu Met  
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 Lys Arg Glu Ile Val Gly Val Val Glu Pro Leu Pro Arg Asp Glu Thr  
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 Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe  
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 Leu Cys Gln Ala Ala Lys Tyr Asn Gly Ser Leu His Lys Cys Asp Ile  
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 Ser Asn Ser Thr Glu Ala Gly Gln Lys Leu Leu Lys Met Leu Ser Leu  
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 Gly Asn Ser Glu Pro Trp Thr Glu Ala Leu Glu Asn Val Val Gly Ala  
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 Arg Asn Met Asp Val Lys Pro Leu Leu Asn Tyr Phe Gln Pro Leu Phe  
 580 585 590  
 Asp Trp Leu Lys Glu Gln Asn Arg Asn Ser Phe Val Gly Trp Asn Thr  
 595 600 605  
 Glu Trp Ser Pro Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu  
 610 615 620  
 Lys Ser Ala Leu Gly Ala Asn Ala Tyr Glu Trp Thr Asn Asn Glu Met  
 625 630 635 640  
 Phe Leu Phe Arg Ser Ser Val Ala Tyr Ala Met Arg Lys Tyr Ser Ser  
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Ile Ile Lys Asn Gln Thr Val Pro Phe Leu Glu Glu Asp Val Arg Val  
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 Ser Asp Leu Lys Pro Arg Val Ser Phe Tyr Phe Phe Val Thr Ser Pro  
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 Gln Asn Val Ser Asp Val Ile Pro Arg Ser Glu Val Glu Asp Ala Ile  
 690 695 700  
 Arg Met Ser Arg Gly Arg Ile Asn Asp Val Phe Gly Leu Asn Asp Asn  
 705 710 715 720  
 Ser Leu Glu Phe Leu Gly Ile His Pro Thr Leu Glu Pro Pro Tyr Gln  
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 Pro Pro Val Thr Ile Trp Leu Ile Ile Phe Gly Val Val Met Ala Leu  
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